

RAW SEQUENCE LISTING

DATE: 01/16/2002

PATENT APPLICATION: US/09/993,234

TIME: 18:33:08

Input Set : N:\Crf3\RULE60\09993234.raw

Output Set: N:\CRF3\01162002\I993234.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

7 (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

9 (iii) NUMBER OF SEQUENCES: 11

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Genentech, Inc.

13 (B) STREET: 460 Point San Bruno Blvd

14 (C) CITY: South San Francisco

15 (D) STATE: California

16 (E) COUNTRY: USA

17 (F) ZIP: 94080

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

C--> 26 (A) APPLICATION NUMBER: US/09/993,234

C--> 27 (B) FILING DATE: 19-Nov-2001

28 (C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: 08/828,683

32 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Marschang, Diane L.

38 (B) REGISTRATION NUMBER: 35,600

39 (C) REFERENCE/DOCKET NUMBER: P1007P1

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 415/225-5416

43 (B) TELEFAX: 415/952-9881

44 (C) TELEX: 910/371-7168

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 181 amino acids

50 (B) TYPE: Amino Acid

51 (D) TOPOLOGY: Linear

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

55 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu

56 1 5 10 15

58 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser

59 20 25 30

61 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu

62 35 40 45

64 Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro

65 50 55 60

67 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln

ENTERED

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68		65		70		75
70	Asp Thr Phe Leu Ala Trp Glu Asn His	His Asn Ser Glu Cys Ala				
71		80		85		90
73	Arg Cys Gln Ala Cys Asp Glu Gln Ala	Ser Gln Val Ala Leu Glu				
74		95		100		105
76	Asn Cys Ser Ala Val Ala Asp Thr Arg	Cys Gly Cys Lys Pro Gly				
77		110		115		120
79	Trp Phe Val Glu Cys Gln Val Ser Gln	Cys Val Ser Ser Ser Pro				
80		125		130		135
82	Phe Tyr Cys Gln Pro Cys Leu Asp Cys	Gly Ala Leu His Arg His				
83		140		145		150
85	Thr Arg Leu Leu Cys Ser Arg Arg Asp	Thr Asp Cys Gly Thr Cys				
86		155		160		165
88	Leu Pro Gly Phe Tyr Glu His Gly Asp	Gly Cys Val Ser Cys Pro				
89		170		175		180

91 Thr

92 181

94 (2) INFORMATION FOR SEQ ID NO: 2:

96 (i) SEQUENCE CHARACTERISTICS:

97 (A) LENGTH: 433 base pairs

98 (B) TYPE: Nucleic Acid

99 (C) STRANDEDNESS: Single

100 (D) TOPOLOGY: Linear

102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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105 CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50
107 TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTC AGAGGCTGCC 100
109 CAGCGGGGCA ACTACCTGAA GGCCCTTGC ACGGAGCCCT GCGCAACTCC 150
111 ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200
113 TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
115 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
117 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350
119 CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
121 ACGGCTAATN TGTTCCCGC AGAGATNATT GTT 433

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123 (2) INFORMATION FOR SEQ ID NO: 3:

125 (i) SEQUENCE CHARACTERISTICS:

126 (A) LENGTH: 28 base pairs

127 (B) TYPE: Nucleic Acid

128 (C) STRANDEDNESS: Single

129 (D) TOPOLOGY: Linear

131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

134 CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

136 (2) INFORMATION FOR SEQ ID NO: 4:

138 (i) SEQUENCE CHARACTERISTICS:

139 (A) LENGTH: 28 base pairs

140 (B) TYPE: Nucleic Acid

141 (C) STRANDEDNESS: Single

142 (D) TOPOLOGY: Linear

144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

147 CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

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149 (2) INFORMATION FOR SEQ ID NO: 5:

151 (i) SEQUENCE CHARACTERISTICS:

152 (A) LENGTH: 1438 base pairs

153 (B) TYPE: Nucleic Acid

154 (C) STRANDEDNESS: Single

155 (D) TOPOLOGY: Linear

157 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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160 GAATTCGCGC GCGGAGGCCG AGAGAGAAAGT CACTTGCCCT GGCTCTACCT 50
162 TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
164 AGCTCTATCC TGTGCCCTGT GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
166 TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
168 CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCCTCC 250
170 CCCCCTCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
172 GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGA 350
174 AGCCCTGGG CGCCCTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
176 GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
178 GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
180 AGATTGGTCT GTTTGTGTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
182 GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCA 600
184 AGACACCTTC TTGGCCTGGG AGAACCACCA TAATCTGAA TGTGCCCCGCT 650
186 GCCAGGCCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
188 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
190 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
192 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
194 GTAGTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
196 CTGCGTGTCC TGCCCCCGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
198 GCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
200 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
202 GTGGGCCCCA CTTAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
204 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACCTTCA GCCAGCATTC 1150
206 CCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
208 GAGTCACATT GATATAGCTT TAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
210 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
212 ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
214 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
216 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

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218 (2) INFORMATION FOR SEQ ID NO: 6:

220 (i) SEQUENCE CHARACTERISTICS:

221 (A) LENGTH: 417 amino acids

222 (B) TYPE: Amino Acid

223 (D) TOPOLOGY: Linear

225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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227 Met Glu Gln Arg Pro Arg Gly Cys Ala Val Ala Ala Ala Leu
228 1 5 10 15
230 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
231 20 25 30
233 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
234 35 40 45
236 Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro

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237		50		55		60
239	Cys Thr Glu Pro Cys Gly Asn Ser Thr		Cys Leu Val Cys Pro Gln			
240		65		70		75
242	Asp Thr Phe Leu Ala Trp Glu Asn His		His Asn Ser Glu Cys Ala			
243		80		85		90
245	Arg Cys Gln Ala Cys Asp Glu Gln Ala		Ser Gln Val Ala Leu Glu			
246		95		100		105
248	Asn Cys Ser Ala Val Ala Asp Thr Arg		Cys Gly Cys Lys Pro Gly			
249		110		115		120
251	Trp Phe Val Glu Cys Gln Val Ser Gln		Cys Val Ser Ser Ser Pro			
252		125		130		135
254	Phe Tyr Cys Gln Pro Cys Leu Asp Cys		Gly Ala Leu His Arg His			
255		140		145		150
257	Thr Arg Leu Leu Cys Ser Arg Arg Asp		Thr Asp Cys Gly Thr Cys			
258		155		160		165
260	Leu Pro Gly Phe Tyr Glu His Gly Asp		Gly Cys Val Ser Cys Pro			
261		170		175		180
263	Thr Ser Thr Leu Gly Ser Cys Pro Glu		Arg Cys Ala Ala Val Cys			
264		185		190		195
266	Gly Trp Arg Gln Met Phe Trp Val Gln		Val Leu Leu Ala Gly Leu			
267		200		205		210
269	Val Val Pro Leu Leu Leu Gly Ala Thr		Leu Thr Tyr Thr Tyr Arg			
270		215		220		225
272	His Cys Trp Pro His Lys Pro Leu Val		Thr Ala Asp Glu Ala Gly			
273		230		235		240
275	Met Glu Ala Leu Thr Pro Pro Pro Ala		Thr His Leu Ser Pro Leu			
276		245		250		255
278	Asp Ser Ala His Thr Leu Leu Ala Pro		Pro Asp Ser Ser Glu Lys			
279		260		265		270
281	Ile Cys Thr Val Gln Leu Val Gly Asn		Ser Trp Thr Pro Gly Tyr			
282		275		280		285
284	Pro Glu Thr Gln Glu Ala Leu Cys Pro		Gln Val Thr Trp Ser Trp			
285		290		295		300
287	Asp Gln Leu Pro Ser Arg Ala Leu Gly		Pro Ala Ala Ala Pro Thr			
288		305		310		315
290	Leu Ser Pro Glu Ser Pro Ala Gly Ser		Pro Ala Met Met Leu Gln			
291		320		325		330
293	Pro Gly Pro Gln Leu Tyr Asp Val Met		Asp Ala Val Pro Ala Arg			
294		335		340		345
296	Arg Trp Lys Glu Phe Val Arg Thr Leu		Gly Leu Arg Glu Ala Glu			
297		350		355		360
299	Ile Glu Ala Val Glu Val Glu Ile Gly		Arg Phe Arg Asp Gln Gln			
300		365		370		375
302	Tyr Glu Met Leu Lys Arg Trp Arg Gln		Gln Gln Pro Ala Gly Leu			
303		380		385		390
305	Gly Ala Val Tyr Ala Ala Leu Glu Arg		Met Gly Leu Asp Gly Cys			
306		395		400		405
308	Val Glu Asp Leu Arg Ser Arg Leu Gln		Arg Gly Pro			
309		410		415		417

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311 (2) INFORMATION FOR SEQ ID NO: 7:
313     (i) SEQUENCE CHARACTERISTICS:
314         (A) LENGTH: 27 base pairs
315         (B) TYPE: Nucleic Acid
316         (C) STRANDEDNESS: Single
317         (D) TOPOLOGY: Linear
319     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
322 GCGGCTCTGG TGGCCCTTGC AGAAGCC 27
324 (2) INFORMATION FOR SEQ ID NO: 8:
326     (i) SEQUENCE CHARACTERISTICS:
327         (A) LENGTH: 25 base pairs
328         (B) TYPE: Nucleic Acid
329         (C) STRANDEDNESS: Single
330         (D) TOPOLOGY: Linear
332     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
335 TTCGGCCGAG AAGTTGAGAA ATGTC 25
337 (2) INFORMATION FOR SEQ ID NO: 9:
339     (i) SEQUENCE CHARACTERISTICS:
340         (A) LENGTH: 1634 base pairs
341         (B) TYPE: Nucleic Acid
342         (C) STRANDEDNESS: Single
343         (D) TOPOLOGY: Linear
345     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
348 CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACACGACG GGCAGAGAGC 50
350 ACGGAGCCGG GAAGCCCTG GGCGCCGTC GGAGGGCT  ATG GAG 94
351                                         Met Glu
352                                         1
354 CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
355 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
356         5                10                15
358 CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
359 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
360         20                25
362 CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
363 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
364         30                35                40
366 AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
367 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
368         45                50
370 CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
371 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
372         55                60                65
374 TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
375 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
376         70                75                80
378 TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
379 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
380         85                90
382 GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09993234.raw

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L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9